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1

Sequence Listing

<110> ZIEGLER, PETRA  
EGGELING, LOTHAR  
SAHM, HERMANN

<120> NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE  
AND PROCESS FOR THE ENZYMATIC PRODUCTION OF  
L-THREONINE USING CORYNEFORM BACTERIA

<130> 21123/282413/MAS

<140> 09/963,521

<141> 2001-09-27

<150> 09/431,099

<151> 1999-11-01

<150> DE 199 41 478.5

<151> 1999-09-01

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 2817

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (398) .. (1864)

<223> thrE-Gen

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tcaagccaaa aagggggcatt ttcattaaga aaataccctt ttgacctggt gttattgagc 180

tggagaagag acttgaactc tcaacctacg cattacaagt gcgttgcgct gccaatgagc 240

ccactccagc accgcagatg ctgatgatca acaactacga atacgtatct tagcgtatgt 300

gtacatcaca atggaattcg gggctagagt atctggtgaa ccgtgcataa acgacctgtg 360

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Met Leu Ser Phe Ala Thr

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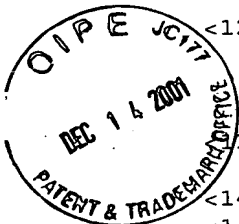
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15

20



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ggc	gtg	atg	aat	ttg	gct	gcg	aga	att	ggc	gat	att	ttg	ctt	tct	tca	559
Gly	Val	Met	Asn	Leu	Ala	Ala	Arg	Ile	Gly	Asp	Ile	Leu	Leu	Ser	Ser	
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ggc	acg	tca	aac	agt	gat	acc	aag	gtg	caa	gtt	cga	gcg	gtg	acc	tct	607
Gly	Thr	Ser	Asn	Ser	Asp	Thr	Lys	Val	Gln	Val	Arg	Ala	Val	Thr	Ser	
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gcg	tat	ggc	ctg	tac	tat	acg	cat	gtg	gat	atc	acg	ttg	aat	acg	atc	655
Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	Ile	Thr	Leu	Asn	Thr	Ile	
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acc	atc	ttc	acc	aac	atc	ggc	gtg	gag	agg	aag	atg	ccg	gtc	aac	gtg	703
Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	Lys	Met	Pro	Val	Asn	Val	
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Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	Phe	Ser	Lys	Leu	Ser	Glu	
		105					110					115				
gtt	gac	cgt	ttg	atc	cgt	tcc	att	cag	gct	ggc	gct	acc	ccg	cct	gag	799
Val	Asp	Arg	Leu	Ile	Arg	Ser	Ile	Gln	Ala	Gly	Ala	Thr	Pro	Pro	Glu	
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gtt	gcc	gag	aaa	att	ctg	gac	gag	ttg	gag	caa	tcg	cct	gcg	tct	tat	847
Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	Gln	Ser	Pro	Ala	Ser	Tyr	
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ggc	ttc	cct	gtt	gag	ttg	ctt	ggc	tgg	gca	atg	atg	ggc	ggc	gct	gtt	895
Gly	Phe	Pro	Val	Ala	Leu	Leu	Gly	Trp	Ala	Met	Met	Gly	Gly	Ala	Val	
				155					160					165		
gct	gtg	ctg	ttg	ggc	ggc	gga	tgg	cag	gtt	tcc	cta	att	gct	ttt	att	943
Ala	Val	Leu	Leu	Gly	Gly	Gly	Trp	Gln	Val	Ser	Leu	Ile	Ala	Phe	Ile	
			170					175					180			
acc	gag	ttc	acg	atc	att	gcc	acg	acg	tca	ttt	ttg	gga	aag	aag	ggc	991
Thr	Ala	Phe	Thr	Ile	Ile	Ala	Thr	Thr	Ser	Phe	Leu	Gly	Lys	Lys	Gly	
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ttg	cct	act	ttc	ttc	caa	aat	gtt	gtt	ggc	ggc	ttt	att	gcc	acg	ctg	1039
Leu	Pro	Thr	Phe	Phe	Gln	Asn	Val	Val	Gly	Gly	Phe	Ile	Ala	Thr	Leu	
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cct	gca	tcg	att	gct	tat	tct	ttg	gag	ttg	caa	ttt	ggc	ctt	gag	atc	1087
Pro	Ala	Ser	Ile	Ala	Tyr	Ser	Leu	Ala	Leu	Gln	Phe	Gly	Leu	Glu	Ile	
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aaa	ccg	agc	cag	atc	atc	gca	tct	gga	att	gtt	gtg	ctg	ttg	gca	ggc	1135
Lys	Pro	Ser	Gln	Ile	Ile	Ala	Ser	Gly	Ile	Val	Val	Leu	Leu	Ala	Gly	
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Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val	
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aca gca agt gca cga ttt ttt gaa aca ctc ctg ttt acc ggc ggc att	1231
Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile	
265 270 275	
gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat gtc	1279
Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val	
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Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr	
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ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca gtg	1375
Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val	
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ggc tgt tac gcg gag tgg tcc tcg gtg att att gcg ggc ctt act gcg	1423
Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala	
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ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc ccc	1471
Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro	
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Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly	
360 365 370	
ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att gcc	1567
Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala	
375 380 385 390	
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Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr	
395 400 405	
gcc acc ttg aat gat caa aca ctc atg ggt ttc acc aac att gcg gtt	1663
Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val	
410 415 420	
gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt gag	1711
Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu	
425 430 435	
tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac cgt	1759
Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg	
440 445 450	
gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag cag	1807
Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln	
455 460 465 470	

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Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly  
475 480 485

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Asn Lys Arg

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<211> 489

<212> PRT

<213> Corynebacterium glutamicum

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Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly  
35 40 45

Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
50 55 60

Val	Arg	Ala	Val	Thr	Ser	Ala	Tyr	Gly	Leu	Tyr	Tyr	Thr	His	Val	Asp	65	70	75	80
Ile	Thr	Leu	Asn	Thr	Ile	Thr	Ile	Phe	Thr	Asn	Ile	Gly	Val	Glu	Arg	85	90	95	
Lys	Met	Pro	Val	Asn	Val	Phe	His	Val	Val	Gly	Lys	Leu	Asp	Thr	Asn	100	105	110	
Phe	Ser	Lys	Leu	Ser	Glu	Val	Asp	Arg	Leu	Ile	Arg	Ser	Ile	Gln	Ala	115	120	125	
Gly	Ala	Thr	Pro	Pro	Glu	Val	Ala	Glu	Lys	Ile	Leu	Asp	Glu	Leu	Glu	130	135	140	
Gln	Ser	Pro	Ala	Ser	Tyr	Gly	Phe	Pro	Val	Ala	Leu	Leu	Gly	Trp	Ala	145	150	155	160
Met	Met	Gly	Gly	Ala	Val	Ala	Val	Leu	Leu	Gly	Gly	Gly	Trp	Gln	Val	165	170	175	
Ser	Leu	Ile	Ala	Phe	Ile	Thr	Ala	Phe	Thr	Ile	Ile	Ala	Thr	Thr	Ser	180	185	190	
Phe	Leu	Gly	Lys	Lys	Gly	Leu	Pro	Thr	Phe	Phe	Gln	Asn	Val	Val	Gly	195	200	205	
Gly	Phe	Ile	Ala	Thr	Leu	Pro	Ala	Ser	Ile	Ala	Tyr	Ser	Leu	Ala	Leu	210	215	220	
Gln	Phe	Gly	Leu	Glu	Ile	Lys	Pro	Ser	Gln	Ile	Ile	Ala	Ser	Gly	Ile	225	230	235	240
Val	Val	Leu	Leu	Ala	Gly	Leu	Thr	Leu	Val	Gln	Ser	Leu	Gln	Asp	Gly	245	250	255	
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Leu	Phe	Thr	Gly	Gly	Ile	Val	Ala	Gly	Val	Gly	Leu	Gly	Ile	Gln	Leu	275	280	285	
Ser	Glu	Ile	Leu	His	Val	Met	Leu	Pro	Ala	Met	Glu	Ser	Ala	Ala	Ala	290	295	300	
Pro	Asn	Tyr	Ser	Ser	Thr	Phe	Ala	Arg	Ile	Ile	Ala	Gly	Gly	Val	Thr	305	310	315	320
Ala	Ala	Ala	Phe	Ala	Val	Gly	Cys	Tyr	Ala	Glu	Trp	Ser	Ser	Val	Ile	325	330	335	
Ile	Ala	Gly	Leu	Thr	Ala	Leu	Met	Gly	Ser	Ala	Phe	Tyr	Tyr	Leu	Phe	340	345	350	
Val	Val	Tyr	Leu	Gly	Pro	Val	Ser	Ala	Ala	Ala	Ile	Ala	Ala	Thr	Ala	355	360	365	

Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
370 375 380

Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
385 390 395 400

Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
405 410 415

Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
420 425 430

Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro  
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Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
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<211> 1909

<212> DNA

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cgccactcca gcaccgcaga tgctgatgat caacaactac gaatacgtat cttagcgtat 180

gtgtacatca caatggaatt cggggctaga gtatctggtg aaccgtgcat aaacgacctg 240

tgattggact ctttttcctt gcaaaatggt ttccagcgg atg ttg agt ttt gcg 294  
Met Leu Ser Phe Ala  
1 5

acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct 342  
Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro  
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ccg cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg 390  
Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val  
25 30 35

gcc ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct	438
Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser	
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tca ggt acg tca aat agt gac acc aag gta caa gtt cga gca gtg acc	486
Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr	
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tct gcg tac ggt ttg tac tac acg cac gtg gat atc acg ttg aat acg	534
Ser Ala Tyr Gly Leu Tyr Thr His Val Asp Ile Thr Leu Asn Thr	
70 75 80 85	
atc acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac	582
Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn	
90 95 100	
gtg ttt cat gtt gta ggc aag ttg gac acc aac ttc tcc aaa ctg tct	630
Val Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser	
105 110 115	
gag gtt gac cgt ttg atc cgt tcc att cag gct ggt gcg acc ccg cct	678
Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala Gly Ala Thr Pro Pro	
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Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser	
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Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala Met Met Gly Gly Ala	
150 155 160 165	
gtt gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt	822
Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe	
170 175 180	
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Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys	
185 190 195	
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Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr	
200 205 210	
ctg cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag	966
Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu	
215 220 225	
atc aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca	1014
Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala	
230 235 240 245	
ggt ttg aca ctc gtg caa tct ctg cag gac ggc atc acg ggc gct ccg	1062
Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro	
250 255 260	





tagaatatcg ggtcgatcgc ttttaaacac tcaggaggat ccttgccggc caaaatcacg 1846  
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<210> 4  
<211> 489  
<212> PRT  
<213> Corynebacterium glutamicum

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Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln  
50 55 60  
Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp  
65 70 75 80  
Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg  
85 90 95  
Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn  
100 105 110  
Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala  
115 120 125  
Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu  
130 135 140  
Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala  
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165 170 175  
Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser  
180 185 190  
Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly  
195 200 205  
Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu  
210 215 220  
Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile  
225 230 235 240

Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly  
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 260 265 270  
 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu  
 275 280 285  
 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala  
 290 295 300  
 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr  
 305 310 315 320  
 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile  
 325 330 335  
 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe  
 340 345 350  
 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala  
 355 360 365  
 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro  
 370 375 380  
 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala  
 385 390 395 400  
 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly  
 405 410 415  
 Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala  
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 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe  
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<212> DNA

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